

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: MSpencer

Timestamp: Mon May 07 12:02:37 EDT 2007

=====

Application No: 10573245

Version No: 1.0

Input Set:

Output Set:

Started: 2007-04-20 12:00:24.452  
Finished: 2007-04-20 12:00:24.973  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 521 ms  
Total Warnings: 1  
Total Errors: 1  
No. of SeqIDs Defined: 24  
Actual SeqID Count: 24

ErrCode	Error Description
E 320	Wrong Nucleic Acid Designator, gab in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)

# SEQUENCE LISTING

<110> The University of York

<120> Expansion Polypeptides

<130> 2902076.1

<140> 10573245

<141> 2007-05-07

<150> 10/573,245

<151> 2006-03-23

<150> PCT/GB04/04058

<151> 2004-08-23

<160> 24

<170> PatentIn version 3.4

<210> 1

<211> 783

<212> DNA

<213> Craterostigma plantagineum

<220>

<221> CDS

<222> (1)..(783)

<400> 1

atg gcg ttt ctg ggc cgc att att att ttt gcg acc ttt ctg gcg att 48

Met Ala Phe Leu Gly Arg Ile Ile Ile Phe Ala Thr Phe Leu Ala Ile

1 5 10 15

acc agc agc agc cat ttt gcg cgc gcg tat tat ggc ggc gat ggc ggc 96

Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly

20 25 30

tgg acc gat gcg cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc 144

Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly

35 40 45

acc atg ggc ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat 192

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr

50 55 60

ggc acc aac acc gcg gcg ctg agc acc gcg ctg ttt aac aac ggc ctg 240

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu

65 70 75 80

agc tgc ggc agc tgc ttt gaa att aaa tgc gcg agc agc att agc ggc 288

Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly

85 90 95

ggc ggc aaa tgg tgc ctg ccg ggc ggc agc att acc gtg acc gcg acc	336
Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr	
100 105 110	
aac ttt tgc ccg ccg aac aac gcg ctg ccg aac aac gcg ggc ggc tgg	384
Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp	
115 120 125	
tgc aac ccg ccg ctg cag cat ttt gat ctg agc cag ccg gtg ttt cag	432
Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln	
130 135 140	
cat att gcg cag tat cgc gcg ggc att gtg ccg gtg agc tat cgc cgc	480
His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg	
145 150 155 160	
gtg ccg tgc cgc cgc cgc ggc ggc att cgc ttt acc att aac ggc cat	528
Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His	
165 170 175	
agc tat ttt aac ctg gtg ctg att acc aac gtg ggc ggc gcg ggc gat	576
Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp	
180 185 190	
gtg cat gcg gtg agc att aaa ggc gcg acc acc gat tgg cag ccg atg	624
Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met	
195 200 205	
agc cgc aac tgg ggc cag aac tgg cag agc aac gcg aac ccg aac ggc	672
Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly	
210 215 220	
cag cgc ctg agc ttt aaa gtg acc acc agc gat ggc cgc acc ctg gtg	720
Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val	
225 230 235 240	
agc aac aac gtg gcg ccg ccg aac tgg agc ttt ggc cag acc ttt gcg	768
Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala	
245 250 255	
ggc gcg cag ttt aac	783
Gly Ala Gln Phe Asn	
260	
<210> 2	
<211> 261	
<212> PRT	
<213> Craterostigma plantagineum	
<400> 2	
Met Ala Phe Leu Gly Arg Ile Ile Ile Phe Ala Thr Phe Leu Ala Ile	
1 5 10 15	
Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly	

20

25

30

Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly  
 35 40 45

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr  
 50 55 60

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu  
 65 70 75 80

Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly  
 85 90 95

Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr  
 100 105 110

Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp  
 115 120 125

Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln  
 130 135 140

His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg  
 145 150 155 160

Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His  
 165 170 175

Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp  
 180 185 190

Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met  
 195 200 205

Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly  
 210 215 220

Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val  
 225 230 235 240

Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala  
 245 250 255

Gly Ala Gln Phe Asn  
260

<210> 3  
<211> 657  
<212> DNA  
<213> *Craterostigma plantagineum*

<220>  
<221> CDS  
<222> (1)..(657)

<400> 3  
gcg acc ttt tat ggc ggc ggc gat gcg agc ggc acc atg ggc ggc gcg 48  
Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala  
1 5 10 15  
tgc ggc tat ggc aac ctg tat agc acc ggc tat ggc acc aac acc gcg 96  
Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala  
20 25 30  
gcg ctg agc acc gcg ctg ttt aac aac ggc ctg acc tgc ggc gcg tgc 144  
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys  
35 40 45  
tat gaa ctg acc tgc aac aac gat ccg cgc ggc tgg tgc ctg agc ggc 192  
Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly  
50 55 60  
acc att atg gtg acc gcg acc aac ttt tgc ccg ccg aac ccg agc ctg 240  
Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu  
65 70 75 80  
ccg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc cag cat ttt gat 288  
Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp  
85 90 95  
ctg gcg gaa ccg gcg ttt ctg cag att gcg cag tat aaa gcg ggc att 336  
Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile  
100 105 110  
gtg ccg gtg aac tat cgc cgc gtg ccg tgc cag aaa aaa ggc ggc att 384  
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile  
115 120 125  
cgc ttt acc att aac ggc cat agc ttt ttt aac ctg gtg ctg gtg acc 432  
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr  
130 135 140  
aac gtg ggc ggc gtg ggc gat gtg cat agc gtg agc att aaa ggc agc 480  
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser  
145 150 155 160

aac ggc ggc tgg cag ccg ctg agc cgc aac tgg ggc cag aac tgg cag	528
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln	
165 170 175	
agc aac agc tat ctg aac ggc cag agc ctg agc ttt cag gtg acc acc	576
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr	
180 185 190	
agc gat ggc cgc acc gtg acc agc tat gat gtg gcg ccg cgc ggc tgg	624
Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp	
195 200 205	
cag ttt ggc cag acc ttt gaa ggc ggc cag ttt	657
Gln Phe Gly Gln Thr Phe Glu Gly Gly Gln Phe	
210 215	
<210> 4	
<211> 219	
<212> PRT	
<213> Craterostigma plantagineum	
<400> 4	
Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala	
1 5 10 15	
Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala	
20 25 30	
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys	
35 40 45	
Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly	
50 55 60	
Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu	
65 70 75 80	
Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp	
85 90 95	
Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile	
100 105 110	
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile	
115 120 125	
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr	

130

135

140

Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser  
 145 150 155 160

Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln  
 165 170 175

Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr  
 180 185 190

Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp  
 195 200 205

Gln Phe Gly Gln Thr Phe Glu Gly Gly Gln Phe  
 210 215

&lt;210&gt; 5

&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Craterostigma plantagineum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(672)

&lt;400&gt; 5

tgc cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc acc atg ggc 48  
 Cys His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly  
 1 5 10 15

ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat ggc acc aac 96  
 Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn  
 20 25 30

acc gcg gcg ctg agc acc acc ctg ttt aac aac ggc ctg gcg tgc ggc 144  
 Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly  
 35 40 45

agc tgc tat cag gtg cgc tgc gaa ggc ggc ccg aaa tgg tgc gtg cgc 192  
 Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg  
 50 55 60

ggc ggc gat cgc att att acc gtg acc gcg acc aac ttt tgc ccg ccg 240  
 Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro  
 65 70 75 80

aac tat gcg ctg gcg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc 288  
 Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg  
 85 90 95



cag cat ttt gat atg gcg cag ccg gcg ttt gtg cgc att gcg cat tat	336
Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr	
100 105 110	
cgc gcg ggc att gtg ccg att agc tat cgc cgc gtg agc tgc gtg aaa	384
Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys	
115 120 125	
aaa ggc ggc att cgc ctg acc att aac ggc cat agc tat ttt aac ctg	432
Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu	
130 135 140	
gtg ctg gtg agc aac gtg ggc ggc agc ggc gat gtg cat gcg gtg tgg	480
Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp	
145 150 155 160	
att aaa ggc agc ggc ggc ggc ccg tgg cag gcg atg acc cgc aac tgg	528
Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp	
165 170 175	
ggc cag aac tgg cag agc aac agc tat ctg gat ggc cag agc ctg agc	576
Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser	
180 185 190	
ttt att gtg cgc gcg ggc gat ggc cgc acc gtg acc gcg aac gab att	624
Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile	
195 200 205	
gtg ccg cgc ggc tgg cag ttt ggc cag acc ttt gaa ggc ccg cag ttt	672
Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe	
210 215 220	

<210> 6  
 <211> 224  
 <212> PRT  
 <213> Craterostigma plantagineum

<220>  
 <221> misc\_feature  
 <222> (207)..(207)  
 <223> The 'Xaa' at location 207 stands for Glu, or Asp.

<400> 6

Cys His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly	
1 5 10 15	
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn	
20 25 30	
Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly	
35 40 45	

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg  
50 55 60

Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro  
65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg  
85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr  
100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys  
115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu  
130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp  
145 150 155 160

Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp  
165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser  
180 185 190

Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile  
195 200 205

Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe  
210 215 220

<210> 7

<211> 8

<212> PRT

<213> Craterostigma plantagineum

<400> 7

Ala Ser Ser Ile Ser Gly Gly Gly  
1 5

<210> 8

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerative primer

<220>  
<221> misc\_feature  
<222> (2)..(2)  
<223> s is Guanine or cytosine

<220>  
<221> misc\_feature  
<222> (3)..(3)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> y is pyrimidine

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<2